RAW SEQUENCE LISTING   DATE: 07/21/2000
PATENT APPLICATION: US/09/202,047   TIME: 11:56:47

Input Set : A:\0020-4491P.APP
Output Set: N:\CRF3\07212000\I202047.raw

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 3 <110> APPLICANT: ITOH, Kyogo
 4        SHICHIJO, Shigeki
 5        IMAI, Yasuhisa
 7 <120> TITLE OF INVENTION: TUMOR ANTIGEN PROTEINS, GENES THEREFOR, AND TUMOR
 8        ANTIGEN PEPTIDES
10 <130> FILE REFERENCE: 0020-4491P
12 <140> CURRENT APPLICATION NUMBER: 09/202,047
13 <141> CURRENT FILING DATE: 1998-12-07
15 <160> NUMBER OF SEQ ID NOS: 2
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2527
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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25 <221> NAME/KEY: 5'UTR
26 <222> LOCATION: (1)..(38)
28 <220> FEATURE:
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30 <222> LOCATION: (39)..(2438)
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38 <222> LOCATION: (2507)..(2527)
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42                                            Met Gly Ser Ser Lys Lys
43                                             1               5
45 cat cgc gga gag aag gag gcg gcc ggg acg acg gcg gcg gcc ggc acc    104
46 His Arg Gly Glu Lys Glu Ala Ala Gly Thr Thr Ala Ala Ala Gly Thr
47              10              15              20
49 ggg ggt gcc acc gag cag ccg ccg cgg cac cgg gaa cac aaa aaa cac   152
50 Gly Gly Ala Thr Glu Gln Pro Pro Arg His Arg Glu His Lys Lys His
51          25              30              35
53 aag cac cgg agt ggc ggc agt ggc ggt agc ggt ggc gaa cga cgg aag   200
54 Lys His Arg Ser Gly Gly Ser Gly Gly Ser Gly Gly Glu Arg Arg Lys
55      40              45              50
57 cgg agc cgg gaa cgt ggg ggc gag cgc ggg agc ggg cgg cgc ggg gcc   248
58 Arg Ser Arg Glu Arg Gly Gly Glu Arg Gly Ser Gly Arg Arg Gly Ala
59  55              60              65              70
61 gaa gct gag gcc cgg agc agc acg cac ggg cgg gag cgc agc cag gca   296
62 Glu Ala Glu Ala Arg Ser Ser Thr His Gly Arg Glu Arg Ser Gln Ala
63              75              80              85
65 gag ccc tcc gag cgg cgc gtg aag cgg gag aag cgc gat gac ggc tac   344
66 Glu Pro Ser Glu Arg Arg Val Lys Arg Glu Lys Arg Asp Asp Gly Tyr
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67               90               95              100
69 gag gcc gct gcc agc tcc aaa act agc tca ggc gat gcc tcc tca ctc   392
70 Glu Ala Ala Ala Ser Ser Lys Thr Ser Ser Gly Asp Ala Ser Ser Leu
71         105              110             115
73 agc atc gag gag act aac aaa ctc cgg gca aag ttg ggg ctg aaa ccc   440
74 Ser Ile Glu Glu Thr Asn Lys Leu Arg Ala Lys Leu Gly Leu Lys Pro
75     120              125             130
77 ttg gag gtt aat gcc atc aag aag gag gcg ggc acc aag gag gag ccc   488
78 Leu Glu Val Asn Ala Ile Lys Lys Glu Ala Gly Thr Lys Glu Glu Pro
79 135              140             145             150
81 gtg aca gct gat gtc atc aac cct atg gcc ttg cga cag cga gag gag   536
82 Val Thr Ala Asp Val Ile Asn Pro Met Ala Leu Arg Gln Arg Glu Glu
83             155             160             165
85 ctg cgg gag aag ctg gcg gct gcc aag gag aag cgc ctg ctg aac caa   584
86 Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu Lys Arg Leu Leu Asn Gln
87         170             175             180
89 aag ctg ggg aag ata aag acc cta gga gag gat gac ccc tgg ctg gac   632
90 Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu Asp Asp Pro Trp Leu Asp
91         185             190             195
93 gac act gca gcc tgg atc gag agg agc cgg cag ctg cag aag gag aag   680
94 Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg Gln Leu Gln Lys Glu Lys
95     200             205             210
97 gac ctg gca gag aag agg gcc aag tta ctg gag gag atg gac caa gag   728
98 Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu Glu Glu Met Asp Gln Glu
99 215             220             225             230
101 ttt ggt gtc agc act ctg gtg gag gag gag ttc ggg cag agg cgg cag  776
102 Phe Gly Val Ser Thr Leu Val Glu Glu Glu Phe Gly Gln Arg Arg Gln
103             235             240             245
105 gac ctg tac agt gcc cgg gac ctg cag ggc ctc acc gtg gag cat gcc  824
106 Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr Val Glu His Ala
107         250             255             260
109 att gat tcc ttc cga gaa ggg gag aca atg att ctt acc ctc aag gac  872
110 Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu Thr Leu Lys Asp
111         265             270             275
113 aaa ggc gtg ctg cag gag gag gag gac gtg ctg gtg aac gtg aac ctg  920
114 Lys Gly Val Leu Gln Glu Glu Glu Asp Val Leu Val Asn Val Asn Leu
115     280             285             290
117 gtg gat aag gag cgg gca gag aaa aat gtg gag ctg cgg aag aag aag  968
118 Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu Arg Lys Lys Lys
119 295             300             305             310
121 cct gac tac ctg ccc tat gcc gag gac gag agc gtg gac gac ctg gcg  1016
122 Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val Asp Asp Leu Ala
123             315             320             325
125 cag caa aaa cct cgc tct atc ctg tcc aag tat gac gaa gag ctt gaa  1064
126 Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp Glu Glu Leu Glu
127             330             335             340
129 ggg gag cgg cca cat tcc ttc cgc ttg gag cag ggc ggc acg gct gat  1112
130 Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly Gly Thr Ala Asp
131             345             350             355
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133 ggc ctg cgg gag cgg gag ctg gag gag atc cgg gcc aag ctg cgg ctg   1160
134 Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala Lys Leu Arg Leu
135     360                 365                 370
137 cag gct cag tcc ctg agc aca gtg ggg ccc cgg ctg gcc tcc gaa tac   1208
138 Gln Ala Gln Ser Leu Ser Thr Val Gly Pro Arg Leu Ala Ser Glu Tyr
139 375                 380                 385                 390
141 ctc acg cct gag atg gtg acc ttt aaa aag acc aag cgg agg gtg       1256
142 Leu Thr Pro Glu Glu Met Val Thr Phe Lys Lys Thr Lys Arg Arg Val
143                 395                 400                 405
145 aag aaa atc cgc aag aag gag aag gag gta gta gtg cgg gca gat gac   1304
146 Lys Lys Ile Arg Lys Lys Glu Lys Glu Val Val Val Arg Ala Asp Asp
147             410                 415                 420
149 ttg ctg cct ctc ggg gac cag act cag gat ggg gac ttt ggt tcc aga   1352
150 Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp Phe Gly Ser Arg
151             425                 430                 435
153 ctg cgg gga cgg ggt cgc cgc cga gtg tcc gaa gtg gag gag gag aag   1400
154 Leu Arg Gly Arg Gly Arg Arg Arg Val Ser Glu Val Glu Glu Glu Lys
155     440                 445                 450
157 gag cct gtg cct cag ccc ctg ccg tcg gac gac acc cga gtg gag aac   1448
158 Glu Pro Val Pro Gln Pro Leu Pro Ser Asp Asp Thr Arg Val Glu Asn
159 455                 460                 465                 470
161 atg gac atc agt gat gag gag gaa ggt gga gct cca ccg ccg ggg tcc   1496
162 Met Asp Ile Ser Asp Glu Glu Glu Gly Gly Ala Pro Pro Pro Gly Ser
163                 475                 480                 485
165 ccg cag gtg ctg gag gag gac gag gcg gag ctg gag ctg cag aag cag   1544
166 Pro Gln Val Leu Glu Glu Asp Glu Ala Glu Leu Glu Leu Gln Lys Gln
167             490                 495                 500
169 ctg gag aag gga cgc cgg ctg cga cag tta cag cag cta cag cag ctg   1592
170 Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu Gln Gln Leu Gln Gln Leu
171         505                 510                 515
173 cga gac agt ggc gag aag gtg gtg gag att gtg aag aag ctg gag tct   1640
174 Arg Asp Ser Gly Glu Lys Val Val Glu Ile Val Lys Lys Leu Glu Ser
175     520                 525                 530
177 cgc cag cgg ggc tgg gag gag gat gag gat ccc gag cgg aag ggg gcc   1688
178 Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp Pro Glu Arg Lys Gly Ala
179 535                 540                 545                 550
181 atc gtg ttc aac gcc acg tcc gag ttc tgc cgc acc ttg ggg gag atc   1736
182 Ile Val Phe Asn Ala Thr Ser Glu Phe Cys Arg Thr Leu Gly Glu Ile
183             555                 560                 565
185 ccc acc tac ggg ctg gct ggc aat cgc gag gag cag gag gag ctc atg   1784
186 Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu Glu Gln Glu Glu Leu Met
187             570                 575                 580
189 gac ttt gaa cgg gat gag gag cgc tca gcc aac ggt ggc tcc gaa tct   1832
190 Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala Asn Gly Gly Ser Glu Ser
191         585                 590                 595
193 gac ggg gag gag aac atc ggc tgg agc acg gtg aac ctg gac gag gag   1880
194 Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr Val Asn Leu Asp Glu Glu
195     600                 605                 610
197 aag cag cag cag gat ttc tct gct tcc tcc acc acc atc ctg gac gag   1928
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198 Lys Gln Gln Gln Asp Phe Ser Ala Ser Ser Thr Thr Ile Leu Asp Glu
199 615                     620                 625                 630
201 gaa ccg atc gtg aat agg ggg ctg gca gct gcc ctg ctc ctg tgt cag    1976
202 Glu Pro Ile Val Asn Arg Gly Leu Ala Ala Ala Leu Leu Leu Cys Gln
203                     635                 640                 645
205 aac aaa ggg ctg ctg gag acc aca gtg cag aag gtg gcc cgg gtg aag    2024
206 Asn Lys Gly Leu Leu Glu Thr Thr Val Gln Lys Val Ala Arg Val Lys
207                     650                 655                 660
209 gcc ccc aac aag tcg ctg ccc tca gcc gtg tac tgc atc gag gat aag    2072
210 Ala Pro Asn Lys Ser Leu Pro Ser Ala Val Tyr Cys Ile Glu Asp Lys
211                     665                 670                 675
213 atg gcc atc gat gac aag tac agc cgg agg gag gaa tac cga ggc ttc    2120
214 Met Ala Ile Asp Asp Lys Tyr Ser Arg Arg Glu Glu Tyr Arg Gly Phe
215         680                 685                 690
217 aca cag gac ttc aag gag aag gac ggc tac aaa ccc gac gtt aag atc    2168
218 Thr Gln Asp Phe Lys Glu Lys Asp Gly Tyr Lys Pro Asp Val Lys Ile
219 695                 700                 705                 710
221 gaa tac gtg gat gag acg ggc cgg aaa ctc aca ccc aag gag gct ttc    2216
222 Glu Tyr Val Asp Glu Thr Gly Arg Lys Leu Thr Pro Lys Glu Ala Phe
223                 715                 720                 725
225 cgg cag ctg tcg cac cgc ttc cat ggc aag ggc tca ggc aag atg aag    2264
226 Arg Gln Leu Ser His Arg Phe His Gly Lys Gly Ser Gly Lys Met Lys
227             730                 735                 740
229 aca gag cgg cgg atg aag aag ctg gac gag gag gcg ctc ctg aag aag    2312
230 Thr Glu Arg Arg Met Lys Lys Leu Asp Glu Glu Ala Leu Leu Lys Lys
231         745                 750                 755
233 atg agc tcc agc gac acg ccc ctg ggc acc gtg gcc ctg ctc cag gag    2360
234 Met Ser Ser Ser Asp Thr Pro Leu Gly Thr Val Ala Leu Leu Gln Glu
235     760                 765                 770
237 aag cag aag gct cag aag acc ccc tac atc gtg ctc agc ggc agc ggc    2408
238 Lys Gln Lys Ala Gln Lys Thr Pro Tyr Ile Val Leu Ser Gly Ser Gly
239 775                 780                 785                 790
241 aag agc atg aac gcg aac acc atc acc aag tgacagcgcc ctcccgtagt    2458
242 Lys Ser Met Asn Ala Asn Thr Ile Thr Lys
243                 795                 800
245 cggccctgcc tcaaccttca tattaaataa agctccctcc ttatttttaa aaaaaaaaaa 2518
247 aaaaaaaaa                                                            2527
250 <210> SEQ ID NO: 2
251 <211> LENGTH: 800
252 <212> TYPE: PRT
253 <213> ORGANISM: Homo sapiens
255 <400> SEQUENCE: 2
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257   1               5                   10                  15
259 Thr Ala Ala Ala Gly Thr Gly Gly Ala Thr Glu Gln Pro Pro Arg His
260             20                  25                  30
262 Arg Glu His Lys Lys His Lys His Arg Ser Gly Gly Ser Gly Gly Ser
263         35                  40                  45
265 Gly Gly Glu Arg Arg Lys Arg Ser Arg Glu Arg Gly Gly Glu Arg Gly
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266      50                    55                  60
268 Ser Gly Arg Arg Gly Ala Glu Ala Glu Ala Arg Ser Ser Thr His Gly
269  65                   70                  75                  80
271 Arg Glu Arg Ser Gln Ala Glu Pro Ser Glu Arg Arg Val Lys Arg Glu
272                  85                  90                  95
274 Lys Arg Asp Asp Gly Tyr Glu Ala Ala Ala Ser Ser Lys Thr Ser Ser
275                 100                 105                 110
277 Gly Asp Ala Ser Ser Leu Ser Ile Glu Glu Thr Asn Lys Leu Arg Ala
278             115                 120                 125
280 Lys Leu Gly Leu Lys Pro Leu Glu Val Asn Ala Ile Lys Lys Glu Ala
281         130                 135                 140
283 Gly Thr Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala
284 145                 150                 155                 160
286 Leu Arg Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu
287                 165                 170                 175
289 Lys Arg Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu
290             180                 185                 190
292 Asp Asp Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg
293         195                 200                 205
295 Gln Leu Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu
296         210                 215                 220
298 Glu Glu Met Asp Gln Glu Phe Gly Val Ser Thr Leu Val Glu Glu Glu
299 225                 230                 235                 240
301 Phe Gly Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly
302                 245                 250                 255
304 Leu Thr Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met
305             260                 265                 270
307 Ile Leu Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Glu Asp Val
308         275                 280                 285
310 Leu Val Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val
311         290                 295                 300
313 Glu Leu Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu
314 305                 310                 315                 320
316 Ser Val Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys
317             325                 330                 335
319 Tyr Asp Glu Glu Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu
320             340                 345                 350
322 Gln Gly Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile
323         355                 360                 365
325 Arg Ala Lys Leu Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro
326         370                 375                 380
328 Arg Leu Ala Ser Glu Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys
329 385                 390                 395                 400
331 Lys Thr Lys Arg Arg Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val
332             405                 410                 415
334 Val Val Arg Ala Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp
335             420                 425                 430
337 Gly Asp Phe Gly Ser Arg Leu Arg Gly Arg Gly Arg Arg Arg Val Ser
338         435                 440                 445
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VERIFICATION SUMMARY                          DATE: 07/21/2000
PATENT APPLICATION:   US/09/202,047           TIME: 11:56:48

Input Set : A:\0020-4491P.APP
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